Replace the paragraph beginning on page 9, line 5, with the following amended paragraph:

B2

--The polynucleotides identified as SEQ ID NO: 1-10, 21-29, 39-46 and 58 contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides or functional portions of polypeptides. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Suitable tools and software for ORF analysis are available, for example, on the Internet. Suitable tools and software for ORF analysis are also available through other distribution channels. Exemplary tools and software include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, open reading frames encoding polypeptides and/or functional portions of polypeptides may be identified using the polynucleotides of the present invention.--

Replace the paragraph beginning on page 11, line 4, with the following amended paragraph:

B3

--Polynucleotide or polypeptide sequences may be aligned, and percentage of identical residues in a specified region may be determined against another polynucleotide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a

protein sequence database. The similarity of polypeptide sequences may be examined using the BLASTP or FASTX algorithms. Both the BLASTN and BLASTP software are available on the NCBI anonymous FTP server and are available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894 USA. The BLASTN algorithm versions 2.0.6 [Sept-16-1998] and version 2.0.11 [Jan-20-2000], set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN and BLASTP, is described at NCBI's website and in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402, 1997.--

B3 cont.

Replace the paragraph beginning on page 11, line 24, with the following amended paragraph:

--The computer algorithm FASTA is available on the Internet. The FASTA software package is also available from the University of Virginia by contacting David Hudson, Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. FASTA Version3.1t11, August 1998, set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, "Improved Tools for Biological Sequence Analysis," *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988 and Pearson, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," *Methods in Enzymol.* 183:63-98, 1990. The use of the FASTX algorithm is described in Pearson *et al.*, "Comparison of DNA sequences with protein sequences," *Genomics* 46:24-36, 1997.--

B4

Replace the paragraph beginning on page 22, line 3, with the following amended paragraph:

--In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most

B5

preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, and potential for formation of loops and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach, CW and Dyksler, GS. *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995.--

B5 CONT.

IN THE CLAIMS:

Cancel claims 24 and 26-28. Add the following new claims:

--29. A method for enhancing an immune response in a patient, comprising:

(a) administering to the patient a composition comprising an isolated polypeptide, wherein the polypeptide comprises SEQ ID NO: 33; and

B6

(b) enhancing an immune response in the patient.

D1

30. The method of claim 29, wherein the composition further comprises at least one component selected from the group consisting of: physiologically acceptable carriers and non-specific immune response enhancers.

31. A method for enhancing an immune response in a patient, comprising:

(a) administering to the patient a composition comprising an isolated polypeptide, wherein the polypeptide comprises a sequence selected from the group consisting of sequences having at least 95% identity to SEQ ID NO: 33 and wherein the polypeptide has the same functional properties as SEQ ID NO: 33; and

(b) enhancing an immune response in the patient.